

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

mail - 15/26/06

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/528,309A
Source: PG/10
Date Processed by STIC: 5/4/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<**<http://www.uspto.gov/ebc/efs/downloads/documents.htm>**> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10/528,309A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."

- 2 Invalid Line Length The rules require that a line **not exceed** 72 characters in length. This includes white spaces.

- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use **space characters**, instead.

- 4 Non-ASCII The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. Please **ensure your subsequent submission is saved in ASCII text**.

- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for **each** skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped
 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If **intentional**, please insert the following lines for **each** skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000

- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.
 In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.

- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence. (see item 11 below)

- 11 Use of <220> Sequence(s) 9 missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules

- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

- 13 Misuse of n/Xaa "n" can **only** represent a single nucleotide; "Xaa" can **only** represent a single amino acid



PCT

RAW SEQUENCE LISTING

DATE: 05/04/2006

PATENT APPLICATION: US/10/528,309A

TIME: 14:13:50

Input Set : A:\SEQLIST 21226Y 08-24-05.TXT

Output Set: N:\CRF4\05042006\J528309A.raw

4 <110> APPLICANT: Clark, Janet
 5 Rohrer, Susan
 6 Alves, Stephen E.
 8 <120> TITLE OF INVENTION: Tryptophan Hydroxylase Assay
 11 <130> FILE REFERENCE: 21226Y
 13 <140> CURRENT APPLICATION NUMBER: 10/528,309A
 14 <141> CURRENT FILING DATE: 2005-03-17
 16 <150> PRIOR APPLICATION NUMBER: 60/412,094
 17 <151> PRIOR FILING DATE: 2002-09-19
 19 <150> PRIOR APPLICATION NUMBER: US03/29320
 20 <151> PRIOR FILING DATE: 2003-09-15
 22 <160> NUMBER OF SEQ ID NOS: 9
 24 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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 29 <213> ORGANISM: Mus Musculus
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 32 <221> NAME/KEY: misc_feature
 33 <222> LOCATION: (0)...(0)
 34 <223> OTHER INFORMATION: Isolate P815 Mouse Mastocytoma cell line, strain
 35 DBA, ATCC Deposit No. TIB-64
 37 <400> SEQUENCE: 1
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 40 tcctctcggt ggactcgccc gatcagctca ctgcgaagga agacgttatg gagactgtcc 180
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 42 gatccgaact tgacgccgac cacc 265
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 47 <213> ORGANISM: Rattus Rattus
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 52 tcctctctgt ggactcgccc gatcagctcc ctgaaaagga agatgttatg gagactgtcc 180
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 54 gatccgaact cgacgccgac cactg 265
 56 <210> SEQ ID NO: 3
 57 <211> LENGTH: 265
 58 <212> TYPE: DNA
 59 <213> ORGANISM: Homo Sapiens
 61 <400> SEQUENCE: 3

p.5

**Does Not Comply
Corrected Diskette Needed**

RAW SEQUENCE LISTING

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64 ttctctctgt gaatctacca gataatttta ctttgaagga agatggatg gaaactgttc 180
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66 gatctgaact agatgcagac cactg                                     265
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76 <223> OTHER INFORMATION: Isolate P815 Mouse Mastocytoma cell, strain DBA
77 ATCC deposit No. TIB-64
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84 cacatcgagt cccggaaaac aaagcaaaga aattcagaat ttgagatatt tgttgactgc 300
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107 tacttctgtt ttgtcttctg gaacctgctg agggaaatat agttcacgtg ccacgtgatg 1680
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111 <211> LENGTH: 1344
112 <212> TYPE: DNA
113 <213> ORGANISM: Mus Musculus
115 <220> FEATURE:

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RAW SEQUENCE LISTING

DATE: 05/04/2006

PATENT APPLICATION: US/10/528,309A

TIME: 14:13:50

Input Set : A:\SEQLIST 21226Y 08-24-05.TXT

Output Set: N:\CRF4\05042006\J528309A.raw

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116 <221> NAME/KEY: misc_feature
117 <222> LOCATION: (0)...(0)
118 <223> OTHER INFORMATION: Isolate P815 Mouse Mastocytoma, cell line, Strain
119     DBA, ATCC, Deposit No. TIB-64
121 <400> SEQUENCE: 5
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124 ttccaggaga atcatgtgag cctgttacac atcgagtccc ggaaatcaaa gcaaagaaat 180
125 tcagaatttg agatatttgg tgactgcgac atcagccgag aacagttgaa tgacatcttc 240
126 cccctgctga agtcgcacgc caccgtcctc tcggtggact cggccgatca gctcactgcg 300
127 aaggaagacg ttatggagac tgtcccttgg tttccaaaga agatttctga cctggacttc 360
128 tgcgccaaaca gagtgtgtgt gtatggatcc gaacttgacg ccgaccaccc tggettcaaa 420
129 gacaatgtct atcgtagaag acgaaagtat tttgcagagt tggtatgaa ctacaaacat 480
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135 ccaggttcag atccctctca cactccagag ccagacacct gccatgaact cctaggccac 840
136 gttcctctct tggctgaacc cagttttgct caattctccc aagaaattgg cctggcttcc 900
137 cttggagctt cagaggagac agttcaaaaa ctggcaacgt gctacttttt cactgtggag 960
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142 ggactgaagt acaaccgcgt cacacagagt gttcagggtc tcagagacac caagagcata 1260
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147 <211> LENGTH: 447
148 <212> TYPE: PRT
149 <213> ORGANISM: Mus Musculus
151 <400> SEQUENCE: 6
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153 1 5 10 15
154 Glu Arg Gly Arg Val Thr Leu Ile Phe Ser Leu Glu Asn Glu Val Gly
155 20 25 30
156 Gly Leu Ile Lys Val Leu Lys Ile Phe Gln Glu Asn His Val Ser Leu
157 35 40 45
158 Leu His Ile Glu Ser Arg Lys Ser Lys Gln Arg Asn Ser Glu Phe Glu
159 50 55 60
160 Ile Phe Val Asp Cys Asp Ile Ser Arg Glu Gln Leu Asn Asp Ile Phe
161 65 70 75 80
162 Pro Leu Leu Lys Ser His Ala Thr Val Leu Ser Val Asp Ser Pro Asp
163 85 90 95
164 Gln Leu Thr Ala Lys Glu Asp Val Met Glu Thr Val Pro Trp Phe Pro
165 100 105 110
166 Lys Lys Ile Ser Asp Leu Asp Phe Cys Ala Asn Arg Val Leu Leu Tyr
167 115 120 125

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168 Gly Ser Glu Leu Asp Ala Asp His Pro Gly Phe Lys Asp Asn Val Tyr
169      130                      135                      140
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171 145                      150                      155                      160
172 Gly Asp Pro Ile Pro Lys Ile Glu Phe Thr Glu Glu Glu Ile Lys Thr
173                      165                      170                      175
174 Trp Gly Thr Ile Phe Arg Glu Leu Asn Lys Leu Tyr Pro Thr His Ala
175                      180                      185                      190
176 Cys Arg Glu Tyr Leu Arg Asn Leu Pro Leu Leu Ser Lys Tyr Cys Gly
177                      195                      200                      205
178 Tyr Arg Glu Asp Asn Ile Pro Gln Leu Glu Asp Val Ser Asn Phe Leu
179      210                      215                      220
180 Lys Glu Arg Thr Gly Phe Ser Ile Arg Pro Val Ala Gly Tyr Leu Ser
181 225                      230                      235                      240
182 Pro Arg Asp Phe Leu Ser Gly Leu Ala Phe Arg Val Phe His Cys Thr
183                      245                      250                      255
184 Gln Tyr Val Arg His Ser Ser Asp Pro Leu Tyr Thr Pro Glu Pro Asp
185                      260                      265                      270
186 Thr Cys His Glu Leu Leu Gly His Val Pro Leu Leu Ala Glu Pro Ser
187                      275                      280                      285
188 Phe Ala Gln Phe Ser Gln Glu Ile Gly Leu Ala Ser Leu Gly Ala Ser
189      290                      295                      300
190 Glu Glu Thr Val Gln Lys Leu Ala Thr Cys Tyr Phe Phe Thr Val Glu
191 305                      310                      315                      320
192 Phe Gly Leu Cys Lys Gln Asp Gly Gln Leu Arg Val Phe Gly Ala Gly
193                      325                      330                      335
194 Leu Leu Ser Ser Ile Ser Glu Leu Lys His Ala Leu Ser Gly His Ala
195                      340                      345                      350
196 Lys Val Lys Pro Phe Asp Pro Lys Ile Ala Cys Lys Gln Glu Cys Leu
197      355                      360                      365
198 Ile Thr Ser Phe Gln Asp Val Tyr Phe Val Ser Glu Ser Phe Glu Asp
199      370                      375                      380
200 Ala Lys Glu Lys Met Arg Glu Phe Ala Lys Thr Val Lys Arg Pro Phe
201 385                      390                      395                      400
202 Gly Leu Lys Tyr Asn Pro Tyr Thr Gln Ser Val Gln Val Leu Arg Asp
203                      405                      410                      415
204 Thr Lys Ser Ile Thr Ser Ala Met Asn Glu Leu Arg Tyr Asp Leu Asp
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210 <210> SEQ ID NO: 7

211 <211> LENGTH: 24

212 <212> TYPE: DNA

213 <213> ORGANISM: Artificial Sequence

215 <220> FEATURE:

216 <223> OTHER INFORMATION: Primer, MTPH-874F

218 <400> SEQUENCE: 7

219 cacagttcag atccccctcta cact

221 <210> SEQ ID NO: 8

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RAW SEQUENCE LISTING

DATE: 05/04/2006

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Input Set : A:\SEQLIST 21226Y 08-24-05.TXT

Output Set: N:\CRF4\05042006\J528309A.raw

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239 20
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needs explanation
(see item 11 on Euro summary sheet)
? what is this?

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VERIFICATION SUMMARY

DATE: 05/04/2006

PATENT APPLICATION: US/10/528,309A

TIME: 14:13:51

Input Set : A:\SEQLIST 21226Y 08-24-05.TXT

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